



SEQUENCE LISTING

<110> De Sauvage, Frederic J.
Klein, Richard D.
Rosenthal, Arnon
Phillips, Heidi S.

<120> GFRALPHA3 AND ITS USES

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<141> 1999-03-19

<150> 60/079,124

<151> 1998-03-23

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<212> DNA

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<213> Mus musculus

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ccacttgag caggaaactc ccttgccaca gagaacagg ttgtgaacag ctgtaccag 180
gccagaaaaga aatgcgaggc taatcccgt tgcaaggctg cctaccagca cctgggctcc 240
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<211> 498

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<213> Mus musculus

<400> 3

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cagcagagga	caagaagctt	aaatccgtcg	ccttcccacc	gttcccagct	ggcagaaact	240
gcttccccaa	acagacggcc	gcccaggtga	ccctcaaggc	catctcggct	cacttcgacg	300
actcgagctc	gtcctcgctg	aagaatgtgt	acttcctgct	cttcgacagc	gagacatcgg	360
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<400> 4

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tcccgtctgc	aaggctgcct	accagcacct	gggtcctgc	acctccagtt	taagcaggcc	300
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aatcctgaac	atttgggcat	gaagagctaa	agtctttggg	tcttgtttaa	ctcctattac	1860
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<210> 5

<211> 397

<212> PRT

<213> Mus musculus

RECEIVED
FEB 04 2002
TECH CENTER 1600/2900

<400> 5

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Thr	Glu	Asn	Arg	Phe	Val	Asn	Ser	Cys	Thr	Gln	Ala	Arg	Lys	Lys	Cys
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Thr	Ser	Ser	Leu	Ser	Arg	Pro	Leu	Pro	Leu	Glu	Glu	Ser	Ala	Met	Ser
65					70					75				80	
Ala	Asp	Cys	Leu	Glu	Ala	Ala	Glu	Gln	Leu	Arg	Asn	Ser	Ser	Leu	Ile
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Asp	Cys	Arg	Cys	His	Arg	Arg	Met	Lys	His	Gln	Ala	Thr	Cys	Leu	Asp
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Ile	Tyr	Trp	Thr	Val	His	Pro	Ala	Arg	Ser	Leu	Gly	Asp	Tyr	Glu	Leu
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Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro	Trp	Lys	Met
	130					135					140				
Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp	Leu	Cys	Leu
145					150					155				160	
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			165						170					175	
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			180					185					190		
Cys	Leu	Ala	Gln	Leu	Arg	Ser	Phe	Phe	Glu	Lys	Ala	Ala	Glu	Ser	His
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Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe	Ile	Ser	Lys
	290					295					300				
Val	Asn	Thr	Thr	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn
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Cys	Leu	Val	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His	Arg	Gln	Leu
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<210> 6

<211> 460

<212> PRT

<213> Homo sapiens

<400> 6

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Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr
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Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly
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145					150					155					160
Ile	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr	Pro	Cys	Thr	Thr	Ser
				165					170					175	
Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg
			180					185					190		
Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser	Tyr	Gly	Met	Leu	Phe
	195					200						205			
Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg	Arg	Arg	Gln	Thr	Ile
	210				215						220				
Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys	Pro	Asn	Cys	Leu	Asn
225					230					235					240
Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys	Arg	Ser	Arg	Leu	Ala
				245					250					255	
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Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn	Asp	Leu	Glu	Glu	Cys
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Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr	Cys	Leu	Lys	Asn	Ala
				325					330					335	
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Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	Thr	Ala	Leu	Arg	Val
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	370					375					380				
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385					390					395					400
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			405						410					415	
Lys	Glu	Gly	Leu	Gly	Ala	Ser	Ser	His	Ile	Thr	Thr	Lys	Ser	Met	Ala
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Ala	Pro	Pro	Ser	Cys	Gly	Leu	Ser	Pro	Leu	Leu	Val	Leu	Val	Val	Thr

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<210> 7
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 <212> PRT
 <213> Homo sapiens

<400> 7

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			20					25					30		
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Ala	Glu	Ser	Asn	Cys	Ser	Ser	Arg	Tyr	Arg	Thr	Leu	Arg	Gln	Cys	Leu
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Ala	Leu	Glu	Val	Leu	Gln	Glu	Ser	Pro	Leu	Tyr	Asp	Cys	Arg	Cys	Lys
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His	Leu	Gly	Leu	Thr	Glu	Gly	Glu	Glu	Phe	Tyr	Glu	Ala	Ser	Pro	Tyr
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Glu	Pro	Val	Thr	Ser	Arg	Leu	Ser	Asp	Ile	Phe	Arg	Leu	Ala	Ser	Ile
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Phe	Ser	Gly	Thr	Gly	Ala	Asp	Pro	Val	Val	Ser	Ala	Lys	Ser	Asn	His
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Cys	Leu	Asp	Ala	Ala	Lys	Ala	Cys	Asn	Leu	Asn	Asp	Asn	Cys	Lys	Lys
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Glu	Arg	Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg	Gln	Phe	Phe
		195					200					205			
Asp	Arg	Val	Pro	Ser	Glu	Tyr	Thr	Tyr	Arg	Met	Leu	Phe	Cys	Ser	Cys
	210					215					220				
Gln	Asp	Gln	Ala	Cys	Ala	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Leu	Pro	Ser
225					230					235					240
Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Gly
				245					250					255	
Val	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	His
			260					265					270		
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Asn	Tyr	Gln	Ala	Cys	Leu	Gly	Ser	Tyr	Ala	Gly	Met	Ile	Gly	Phe	Asp
	290					295					300				
Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Ser	Pro	Thr	Gly	Ile	Val	Val	Ser
305					310					315					320
Pro	Trp	Cys	Ser	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	Cys	Glu
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Gln	Ala	Phe	Gly	Asn	Gly	Thr	Asp	Val	Asn	Val	Ser	Pro	Lys	Gly	Pro
		355					360						365		

Ser	Phe	Gln	Ala	Thr	Gln	Ala	Pro	Arg	Val	Glu	Lys	Thr	Pro	Ser	Leu
	370					375					380				
Pro	Asp	Asp	Leu	Ser	Asp	Ser	Thr	Ser	Leu	Gly	Thr	Ser	Val	Ile	Thr
385					390					395					400
Thr	Cys	Thr	Ser	Val	Gln	Glu	Gln	Gly	Leu	Lys	Ala	Asn	Asn	Ser	Lys
				405					410					415	
Glu	Leu	Ser	Met	Cys	Phe	Thr	Glu	Leu	Thr	Thr	Asn	Ile	Ile	Pro	Gly
			420					425					430		
Ser	Asn	Lys	Val	Ile	Lys	Pro	Asn	Ser	Gly	Pro	Ser	Arg	Ala	Arg	Pro
	435						440					445			
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	450					455					460				

<210> 8

<211> 468

<212> PRT

<213> Rattus norvegicus

<400> 8

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			20					25					30		
Ser	Asp	Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg	Thr
		35					40					45			
Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe	Ser	Leu	Thr	Ser
	50					55				60					
Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg	Ser	Ala	Met	Glu	Ala	Leu	Lys
65					70					75					80
Gln	Lys	Ser	Leu	Tyr	Asn	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu
			85						90					95	
Lys	Asn	Cys	Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly
			100					105					110		
Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn	Ser	Arg	Leu
		115					120					125			
Ser	Asp	Ile	Phe	Arg	Ala	Val	Pro	Phe	Ile	Ser	Asp	Val	Phe	Gln	Gln
	130					135					140				
Val	Glu	His	Ile	Ser	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala
145					150					155					160
Cys	Asn	Leu	Asp	Asp	Thr	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr
			165						170					175	
Pro	Cys	Thr	Thr	Ser	Met	Ser	Asn	Glu	Val	Cys	Asn	Arg	Arg	Lys	Cys
			180					185					190		
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser
	195						200					205			
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg
	210					215					220				
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Arg
225					230					235					240
Pro	Asn	Cys	Leu	Ser	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys
			245						250					255	
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg
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Ser	Val	Ser	Asn	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala
	275						280					285			
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser

290		295		300
Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn				
305		310		315
Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr				
		325		330
				335
Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr				
		340		345
				350
Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr Thr				
		355		360
				365
Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu				
		370		375
				380
Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala				
385		390		395
				400
Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr His Leu Cys Leu Ser				
		405		410
				415
Asp Ser Asp Phe Gly Lys Asp Gly Leu Ala Gly Ala Ser Ser His Ile				
		420		425
				430
Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser Leu				
		435		440
				445
Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser Leu				
		450		455
				460
Ala Glu Thr Ser				
465				

<210> 9

<211> 464

<212> PRT

<213> Rattus Norvegicus

<400> 9

Met Ile Leu Ala Asn Ala Phe Cys Leu Phe Phe Phe Leu Asp Glu Thr				
1		5		10
				15
Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Ser Glu Leu His				
		20		25
				30
Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala				
		35		40
				45
Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu				
		50		55
				60
Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala				
65		70		75
				80
Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys				
		85		90
				95
Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile				
		100		105
				110
His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr				
		115		120
				125
Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile				
		130		135
				140
Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn His				
145		150		155
				160
Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys				
		165		170
				175
Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr				
		180		185
				190
Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe				
		195		200
				205

Asp	Arg	Val	Pro	Ser	Glu	Tyr	Thr	Tyr	Arg	Met	Leu	Phe	Cys	Ser	Cys	210	215	220
Gln	Asp	Gln	Ala	Cys	Ala	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Leu	Pro	Ser	225	230	235
Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Ser	240	245	250
Leu	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	His	255	260	265
Ala	Asn	Cys	Arg	Ala	Ser	Tyr	Arg	Thr	Ile	Thr	Ser	Cys	Pro	Ala	Asp	270	275	280
Asn	Tyr	Gln	Ala	Cys	Leu	Gly	Ser	Tyr	Ala	Gly	Met	Ile	Gly	Phe	Asp	285	290	295
Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Asn	Pro	Thr	Gly	Ile	Val	Val	Ser	300	305	310
Pro	Trp	Cys	Asn	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	Cys	Glu	315	320	325
Lys	Phe	Leu	Arg	Asp	Phe	Thr	Glu	Asn	Pro	Cys	Leu	Arg	Asn	Ala	Ile	330	335	340
Gln	Ala	Phe	Gly	Asn	Gly	Thr	Asp	Val	Asn	Met	Ser	Pro	Lys	Gly	Pro	345	350	355
Ser	Leu	Pro	Ala	Thr	Gln	Ala	Pro	Arg	Val	Glu	Lys	Thr	Pro	Ser	Leu	360	365	370
Pro	Asp	Asp	Leu	Ser	Asp	Ser	Thr	Ser	Leu	Gly	Thr	Ser	Val	Ile	Thr	375	380	385
Thr	Cys	Thr	Ser	Ile	Gln	Glu	Gln	Gly	Leu	Lys	Ala	Asn	Asn	Ser	Lys	390	395	400
Glu	Leu	Ser	Met	Cys	Phe	Thr	Glu	Leu	Thr	Thr	Asn	Ile	Ser	Pro	Gly	405	410	415
Ser	Lys	Lys	Val	Ile	Lys	Leu	Asn	Ser	Gly	Ser	Ser	Arg	Ala	Arg	Leu	420	425	430
Ser	Ala	Ala	Leu	Thr	Ala	Leu	Pro	Leu	Leu	Met	Leu	Thr	Leu	Ala	Leu	435	440	445
																450	455	460

<210> 10
 <211> 282
 <212> DNA
 <213> Homo sapiens

<220>

<221> unsure
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 cccctgaacc cgcgaccgct gccgccgta gnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180
 nnnnnnnngc ctctcgcagc cggagacccc cttccacag aaagccgact catgaacagc 240
 tgtctccagg ccaggaggaa gtgccaggct gatccacct gc 282

<210> 11
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 11
gcctctcgca gccggagacc 20

<210> 12
<211> 21
<212> DNA
<213> Homo sapiens

<400> 12
caggtgggat cagcctggca c 21

<210> 13
<211> 41
<212> DNA
<213> Homo sapiens

<400> 13
tctcgagcc ggagaccccc ttccacaga aagccgactc a 41

<210> 14
<211> 1792
<212> DNA
<213> Homo sapiens

<400> 14
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atgaacagct gtctccaggc caggaggaag tgccaggctg atcccacctg cagtgctgcc 180
taccaccacc tggattcctg cacctctagc ataagcacc cactgccctc agaggagcct 240
tcggtccttg ctgactgcct ggaggcagca cagcaactca ggaacagctc tctgataggc 300
tgcatgtgcc accggcgcat gaagaaccag gttgcctgct tggacatcta ttggaccgtt 360
caccgtgccc gcagccttgg taactatgag ctggtgtct cccctatga agacacagtg 420
accagcaaac cctggaaaaa gaatctcagc aaactgaaca tgctcaaacc agactcagac 480
ctctgcctca agtttgccat gctgtgtact ctcaatgaca agtgtgaccg gctgcgcaag 540
gcctacgggg aggcgtgctc cgggccccac tgccagcgcc acgtctgcct caggcagctg 600
ctcactttct tcgagaaggc cgccgagccc cagcgcgagg gctgctact gtgcccattg 660
gcccccaacg accggggctg cggggagcgc cggcgcaaca ccacgcccc caactgcgcg 720
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tgcagatcac gcctggtgga ttccagacc cactgccatc ccattggacat cctaggaact 840
tgtgcaacag agcagtcag atgtctacga gcatacctg ggctgattgg gactgccatg 900
acccccaaact ttgtcagcaa tgtcaacacc agtgttgccct taagctgcac ctgccgaggc 960
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ccacacccta cctttgctgt gatggcacac cagaatgaaa accctgctgt gaggccacag 1140
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caaggggtga ggaaaggaca gcagcaggaa ggagggtgag tgcgcagatg agggcacagg 1320
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agaatctaât aagttagcct ttctctattg cattccagat tagggttagg gtagggagga 1560
ctgggtgttc tgaggcagcc tagaaagtca ttctcctttg tgaagaaggc tcctgcccc 1620
tcgtctcctc ctctgagtgg aggatggaaa actactgcct gcactgccct gtccccgat 1680
cctgccgaac atctgggcat caggagctgg agcctgtggg ccttgcttta ttctattat 1740
tgtcctaaag tctctctggg ctcttgatc atgattaaac ctttgactta ag 1792

<210> 15

<211> 400
 <212> PRT
 <213> Homo Sapiens

<400> 15

Met	Val	Arg	Pro	Leu	Asn	Pro	Arg	Pro	Leu	Pro	Pro	Val	Val	Leu	Met
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Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ser	Pro	Leu	Pro	Leu	Ala	Ala	Gly	Asp
			20					25					30		
Pro	Leu	Pro	Thr	Glu	Ser	Arg	Leu	Met	Asn	Ser	Cys	Leu	Gln	Ala	Arg
		35					40					45			
Arg	Lys	Cys	Gln	Ala	Asp	Pro	Thr	Cys	Ser	Ala	Ala	Tyr	His	His	Leu
50						55					60				
Asp	Ser	Cys	Thr	Ser	Ser	Ile	Ser	Thr	Pro	Leu	Pro	Ser	Glu	Glu	Pro
65					70					75					80
Ser	Val	Pro	Ala	Asp	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser
				85					90					95	
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
			100					105					110		
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
		115					120					125			
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
		130				135					140				
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
145					150					155					160
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
				165					170					175	
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
			180					185					190		
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala
		195					200					205			
Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp	
		210				215				220					
Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala
225					230					235					240
Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe
				245					250					255	
Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys
			260					265					270		
His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys
		275					280					285			
Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe
						295					300				
Val	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly
305					310					315					320
Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser
				325					330					335	
His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His
			340					345					350		
Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met
		355					360					365			
Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro
		370				375					380				
Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp
385					390					395					400

<210> 16
 <211> 1837
 <212> DNA
 <213> Homo sapeins

<400> 16
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 ggtgccggtc gagggagccc cgctctcaga gctccagggg aggagcgagg ggagcgcgga 120
 gcccggcgcc tacagctcgc catggtgctg cccctgaacc cgcgaccgct gccgcccgtg 180
 gtctctgatgt tgctgctgct gctgccgccc tcgccgctgc ctctcgcagc cggagacccc 240
 cttccacag aaagccgact catgaacagc tgtctccagg ccaggaggaa gtgccaggct 300
 gatccacct gcagtgtgc ctaccaccac ctggattcct gcacctctag cataagcacc 360
 ccactgccct cagaggagcc ttccggtccct gctgactgcc tggaggcagc acagcaactc 420
 aggaacagct ctctgatagg ctgcatgtgc caccggcgca tgaagaacca ggttgcctgc 480
 ttggacatct attggaccgt tcaccgtgcc cgcagccttg actcagacct ctgcctcaag 540
 tttgccatgc tgtgtactct caatgacaag tgtgaccggc tgcgcaaggc ctacggggag 600
 gcgtgctccg ggccccactg ccagcgccac gtctgcctca ggcagctgct cactttcttc 660
 gagaaggccg ccgagcccca cgcgcagggc ctgctactgt gcccatgtgc ccccaacgac 720
 cggggctgcg gggagcgccg gcgcaacacc atcgcccca actgcgcgct gccgcctgtg 780
 gcccccaact gcctggagct gcggcgctc tgccttctccg acccgcttg cagatcacgc 840
 ctggtggatt tccagaccca ctgccatccc atggacatcc taggaacttg tgcaacagag 900
 cagtccagat gtctacgagc atacctgggg ctgattggga ctgccatgac cccaacttt 960
 gtcagcaatg tcaacaccag tgttcctta agctgcacct gccgaggcag tggcaacctg 1020
 caggaggagt gtgaaatgct ggaagggttc ttctccaca acccctgcct cacggaggcc 1080
 attgcagcta agatgcgttt tcacagccaa ctcttctccc aggactggcc acaccctacc 1140
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 tctcttttct cctgcacgct tcccttgatt ctgctcctga gcctatggta gctggacttc 1260
 cccaggggcc tcttcccctc caccacaccc aggtggactt gcagcccaca aggggtgagg 1320
 aaaggacagc agcaggaagg aggtgcagt cgcagatgag ggcacaggag aagctaaggg 1380
 ttatgacctc cagatcctta ctggtccagt cctcattccc tccaccccat ctccacttct 1440
 gattcatgct gccctcctt ggtggccaca atttagccat gtcatctggt ggtgaccagc 1500
 tccaccaagc ccctttctga gcccttctc ttgactacca ggatcaccag aatctaataa 1560
 gttagccttt ctctattgca ttcagatta ggggtagggt agggaggact ggggtgttctg 1620
 aggcagccta gaaagtccatt ctcccttctg aagaaggctc ctgccccctc gtctcctcct 1680
 ctgagtggag gatgaaaac tactgcctgc actgccctgt ccccgatcc tgccgaacat 1740
 ctgggcatca ggagctggag cctgtgggcc ttgctttatt cctattattg tcctaaagtc 1800
 tctctgggct cttggatcat gattaaacct ttgactt 1837

<210> 17
 <211> 369
 <212> PRT
 <213> Homo sapiens

<400> 17
 Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
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 Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
 20 25 30
 Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
 35 40 45
 Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
 50 55 60
 Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
 65 70 75 80
 Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
 85 90 95
 Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala

				85				90					95				
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala		
			100					105					110				
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn		
		115					120					125					
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro		
	130					135					140						
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp		
145					150					155					160		
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp		
			165						170					175			
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln		
			180					185					190				
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala		
		195				200						205					
Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp		
	210					215					220						
Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala		
225					230					235					240		
Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe		
			245						250					255			
Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys		
			260					265					270				
His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys		
		275					280					285					
Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe		
	290					295					300						
Val	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly		
305					310					315					320		
Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser		
			325						330					335			
His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His		
			340					345					350				
Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met		
		355				360						365					
Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro		
	370					375					380						
Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp		
385					390					395					400		
Pro	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu		
			405						410					415			
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu		
			420					425					430				
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser		
		435					440					445					
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu		
	450					455					460						
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr		
465					470					475					480		
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn		
			485						490					495			
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro		
			500					505					510				
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln		
		515					520					525					
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val		
	530					535					540						

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 545 550 555 560
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 565 570 575
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 580 585 590
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 595 600 605
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 610 615 620
 Ser Pro Gly Lys
 625

<210> 19

<211> 951

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric receptor comprising rat sequence.

<400> 19

Met Gly Gly Thr Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val Val
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 Ile Val Gly Leu His Gly Val Arg Gly Lys Tyr Ala Leu Ala Asp Ala
 20 25 30
 Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro
 35 40 45
 Val Leu Asp Gln Leu Leu Glu Pro Ser Ser Leu Gln Gly Ser Glu Leu
 50 55 60
 His Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu Leu Cys
 65 70 75 80
 Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys
 85 90 95
 Leu Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln
 100 105 110
 Ala Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys
 115 120 125
 Lys Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser
 130 135 140
 Ile His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro
 145 150 155 160
 Tyr Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser
 165 170 175
 Ile Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn
 180 185 190
 His Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys
 195 200 205
 Lys Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro
 210 215 220
 Thr Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe
 225 230 235 240
 Phe Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser
 245 250 255
 Cys Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro
 260 265 270

Ser	Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg
		275					280					285			
Ser	Leu	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe
	290					295					300				
His	Ala	Asn	Cys	Arg	Ala	Ser	Tyr	Arg	Thr	Ile	Thr	Ser	Cys	Pro	Ala
305					310					315					320
Asp	Asn	Tyr	Gln	Ala	Cys	Leu	Gly	Ser	Tyr	Ala	Gly	Met	Ile	Gly	Phe
				325					330					335	
Asp	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Asn	Pro	Thr	Gly	Ile	Val	Val
			340					345					350		
Ser	Pro	Trp	Cys	Asn	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	Cys
		355					360					365			
Glu	Lys	Phe	Leu	Arg	Asp	Phe	Thr	Glu	Asn	Pro	Cys	Leu	Arg	Asn	Ala
	370					375					380				
Ile	Gln	Ala	Phe	Gly	Asn	Gly	Thr	Asp	Val	Asn	Met	Ser	Pro	Lys	Gly
385					390					395					400
Pro	Ser	Leu	Pro	Ala	Thr	Gln	Ala	Pro	Arg	Val	Glu	Lys	Thr	Pro	Ser
				405					410					415	
Leu	Pro	Asp	Asp	Leu	Ser	Asp	Ser	Thr	Ser	Leu	Gly	Thr	Ser	Val	Ile
			420					425					430		
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